SEQUENCE LISTING

```
<110>   CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
<110>   BIONOSTRA, S.L.

<120>   CHIMERIC EMPTY CAPSIDS OF THE INFECTIOUS BURSAL DISEASE VIRUS
        (IBDV), OBTAINMENT PROCESS AND APPLICATIONS

<130>   P1391PC

<150>   ES P200400120
<151>   2004-01-21 (January 21, 2004)

<160>   14

<170>   PatentIn version 3.1


<210>   1
<211>   35
<212>   DNA
<213>   Artificial sequence

<220>   Synthetic DNA
<223>   Oligo I primer

<400>   1
gcgcagatct atgacaaacc tgtcagatca aaccc                                   35


<210>   2
<211>   34
<212>   DNA
<213>   Artificial sequence

<220>   Synthetic DNA
<223>   Oligo II primer

<400>   2
gcgcaagctt aggcgagagt cagctgcctt atgc                                    34


<210>   3
<211>   7595
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Plasmid pFBD/pVP2-his-VP3

<220>
<221>   promoter
<222>   (157)..(285)
<223>   Promoter ppolh

<220>
<221>   CDS
<222>   (291)..(1289)
<223>   pVP2 ORF
```

```
<220>
<221>   promoter
<222>   (7443)..(7503)
<223>   Promoter p10

<400>   3
gggtgatcaa gtcttcgtcg agtgattgta aataaaatgt aatttacagt atagtatttt      60

aattaatata caaatgattt gataataatt cttatttaac tataatatat tgtgttgggt     120

tgaattaaag gtccgtatac tccggaatat taatagatca tggagataat taaaatgata     180

accatctcgc aaataaataa gtattttact gttttcgtaa cagttttgta ataaaaaaac     240

ctataaatat tccggattat tcataccgtc ccaccatcgg gcgcggatct atg aca        296
                                                        Met Thr
                                                        1

aac ctg tca gat caa acc cag cag att gtt ccg ttc ata cgg agc ctt       344
Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg Ser Leu
        5                   10                  15

ctg atg cca aca acc gga ccg gcg tcc att ccg gac gac acc ctg gag       392
Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr Leu Glu
        20                  25                  30

aag cac act ctc agg tca gag acc tcg acc tac aat ttg act gtg ggg       440
Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr Val Gly
35                  40                  45                  50

gac aca ggg tca ggg cta att gtc ttt ttc cct gga ttc cct ggc tca       488
Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro Gly Ser
                55                  60                  65

att gtg ggt gct cac tac aca ctg cag ggc aat ggg aac tac aag ttc       536
Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr Lys Phe
                70                  75                  80

gat cag atg ctc ctg act gcc cag aac cta ccg gcc agt tac aac tac       584
Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr Asn Tyr
            85                  90                  95

tgc agg cta gtg agt cgg agt ctc aca gtg agg tca agc aca ctt cct       632
Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr Leu Pro
            100                 105                 110

ggt ggc gtt tat gca cta aac ggc acc ata aac gcc gtg acc ttc caa       680
Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr Phe Gln
115                 120                 125                 130

gga agc ctg agt gaa ctg aca gat gtt agc tac aat ggg ttg atg tct       728
Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu Met Ser
                135                 140                 145

gca aca gcc aac atc aac gac aaa att ggg aac gtc cta gta ggg gaa       776
Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val Gly Glu
                150                 155                 160
```

```
ggg gtc acc gtc ctc agc tta ccc aca tca tat gat ctt ggg tat gtg     824
Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly Tyr Val
        165                 170                 175

agg ctt ggt gac ccc att ccc gca ata ggg ctt gac cca aaa atg gta     872
Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys Met Val
        180                 185                 190

gcc aca tgt gac agc agt gac agg ccc aga gtc tac acc ata act gca     920
Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile Thr Ala
195                 200                 205                 210

gcc gat gat tac caa ttc tca tca cag tac caa cca ggt ggg gta aca     968
Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly Val Thr
                215                 220                 225

atc aca ctg ttc tca gcc aac att gat gcc atc aca agc ctc agc gtt    1016
Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu Ser Val
                230                 235                 240

ggg gga gag ctc gtg ttt cga aca agc gtc cac ggc ctt gta ctg ggc    1064
Gly Gly Glu Leu Val Phe Arg Thr Ser Val His Gly Leu Val Leu Gly
        245                 250                 255

gcc acc atc tac ctc ata ggc ttt gat ggg aca acg gta atc acc agg    1112
Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile Thr Arg
        260                 265                 270

gct gtg gcc gca aac aat ggg ctg acg acc ggc acc gac aac ctt atg    1160
Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn Leu Met
275                 280                 285                 290

cca ttc aat ctt gtg att cca aca aac gag ata acc cag cca atc aca    1208
Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro Ile Thr
                295                 300                 305

tcc atc aaa ctg gag ata gtg acc tcc aaa agt ggt ggt cag gca ggg    1256
Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln Ala Gly
        310                 315                 320

gat cag atg tca tgg tcg gca aga ggg agc cta gcagtgacga tccatggtgg   1309
Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu
        325                 330

caactatcca ggggccctcc gtcccgtcac gctagtggcc tacgaaagag tggcaacagg    1369

atccgtcgtt acggtcgctg gggtgagcaa cttcgagctg atcccaaatc ctgaactagc    1429

aaagaacctg gttacagaat acggccgatt tgacccagga gccatgaact acacaaaatt    1489

gatactgagt gagagggacc gtcttggcat caagaccgtc tggccaacaa gggagtacac    1549

tgactttcgt gaatacttca tggaggtggc cgacctcaac tctcccctga gattgcagg    1609

agcattcggc ttcaaagaca taatccgggc cataaggagg atagctgtgc cggtggtctc    1669

cacattgttc ccacctgccg ctcccctagc ccatgcaatt ggggaaggtg tagactacct    1729

gctgggcgat gaggcccagg ccgcttcagg aactgctcga ccgcgtcag gaaaagcaag    1789
```

```
agctgcctca ggccgcataa ggcagctgac tctcgcctaa gcttgtcgag aagtactaga   1849

ggatcataat cagccatacc acatttgtag aggttttact tgctttaaaa aacctcccac   1909

acctccccct gaacctgaaa cataaaatga atgcaattgt tgttgttaac ttgtttattg   1969

cagcttataa tggttacaaa taaagcaata gcatcacaaa tttcacaaat aaagcatttt   2029

tttcactgca ttctagttgt ggtttgtcca aactcatcaa tgtatcttat catgtctgga   2089

tctgatcact gcttgagcct aggagatccg aaccagataa gtgaaatcta gttccaaact   2149

attttgtcat ttttaatttt cgtattagct tacgacgcta cacccagttc ccatctattt   2209

tgtcactctt ccctaaataa tccttaaaaa ctccatttcc acccctccca gttcccaact   2269

attttgtccg cccacagcgg ggcatttttc ttcctgttat gtttttaatc aaacatcctg   2329

ccaactccat gtgacaaacc gtcatcttcg gctacttttt ctctgtcaca gaatgaaaat   2389

ttttctgtca tctcttcgtt attaatgttt gtaattgact gaatatcaac gcttatttgc   2449

agcctgaatg gcgaatggga cgcgccctgt agcggcgcat taagcgcggc gggtgtggtg   2509

gttacgcgca gcgtgaccgc tacacttgcc agcgccctag cgcccgctcc tttcgctttc   2569

ttcccttcct ttctcgccac gttcgccggc tttccccgtc aagctctaaa tcggggctc   2629

cctttagggt tccgatttag tgctttacgg cacctcgacc ccaaaaaact tgattagggt   2689

gatggttcac gtagtgggcc atcgccctga tagacggttt ttcgcccttt gacgttggag   2749

tccacgttct ttaatagtgg actcttgttc caaactggaa caacactcaa ccctatctcg   2809

gtctattctt ttgatttata agggattttg ccgatttcgg cctattggtt aaaaaatgag   2869

ctgatttaac aaaaatttaa cgcgaatttt aacaaaatat taacgtttac aatttcaggt   2929

ggcacttttc ggggaaatgt gcgcggaacc cctatttgtt tattttttcta aatacattca   2989

aatatgtatc cgctcatgag acaataaccc tgataaatgc ttcaataata ttgaaaaagg   3049

aagagtatga gtattcaaca tttccgtgtc gcccttattc cctttttttgc ggcattttgc   3109

cttcctgttt ttgctcaccc agaaacgctg gtgaaagtaa aagatgctga agatcagttg   3169

ggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct tgagagtttt   3229

cgccccgaag aacgttttcc aatgatgagc acttttaaag ttctgctatg tggcgcggta   3289

ttatcccgta ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat   3349

gacttggttg agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga   3409

gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca   3469

acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact   3529

cgccttgatc gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc   3589
```

```
acgatgcctg tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact   3649

ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt   3709

ctgcgctcgg cccttccggc tggctggttt attgctgata aatctggagc cggtgagcgt   3769

gggtctcgcg gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt   3829

atctacacga cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata   3889

ggtgcctcac tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag   3949

attgatttaa aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat   4009

ctcatgacca aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa   4069

aagatcaaag gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca   4129

aaaaaaccac cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt   4189

ccgaaggtaa ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg   4249

tagttaggcc accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc   4309

ctgttaccag tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga   4369

cgatagttac cggataaggc gcagcggtcg ggctgaacgg ggggttcgtg cacacagccc   4429

agcttggagc gaacgaccta caccgaactg agatacctac agcgtgagca ttgagaaagc   4489

gccacgcttc ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca   4549

ggagagcgca cgagggagct tccaggggga aacgcctggt atctttatag tcctgtcggg   4609

tttcgccacc tctgacttga gcgtcgattt ttgtgatgct cgtcaggggg cggagccta    4669

tggaaaaacg ccagcaacgc ggccttttta cggttcctgg ccttttgctg gccttttgct   4729

cacatgttct ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag   4789

tgagctgata ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa   4849

gcggaagagc gcctgatgcg gtattttctc cttacgcatc tgtgcggtat ttcacaccgc   4909

agaccagccg cgtaacctgg caaaatcggt tacggttgag taataaatgg atgccctgcg   4969

taagcgggtg tgggcggaca ataaagtctt aaactgaaca aaatagatct aaactatgac   5029

aataaagtct taaactagac agaatagttg taaactgaaa tcagtccagt tatgctgtga   5089

aaaagcatac tggacttttg ttatggctaa agcaaactct tcattttctg aagtgcaaat   5149

tgcccgtcgt attaaagagg ggcgtggcca agggcatggt aaagactata ttcgcggcgt   5209

tgtgacaatt taccgaacaa ctccgcggcc gggaagccga tctcggcttg aacgaattgt   5269

taggtggcgg tacttgggtc gatatcaaag tgcatcactt cttcccgtat gcccaacttt   5329

gtatagagag ccactgcggg atcgtcaccg taatctgctt gcacgtagat cacataagca   5389
```

```
ccaagcgcgt  tggcctcatg  cttgaggaga  ttgatgagcg  cggtggcaat  gccctgcctc    5449

cggtgctcgc  cggagactgc  gagatcatag  atatagatct  cactacgcgg  ctgctcaaac    5509

ctgggcagaa  cgtaagccgc  gagagcgcca  acaaccgctt  cttggtcgaa  ggcagcaagc    5569

gcgatgaatg  tcttactacg  gagcaagttc  ccgaggtaat  cggagtccgg  ctgatgttgg    5629

gagtaggtgg  ctacgtctcc  gaactcacga  ccgaaaagat  caagagcagc  ccgcatggat    5689

ttgacttggt  cagggccgag  cctacatgtg  cgaatgatgc  ccatacttga  gccacctaac    5749

tttgttttag  ggcgactgcc  ctgctgcgta  acatcgttgc  tgctgcgtaa  catcgttgct    5809

gctccataac  atcaaacatc  gacccacggc  gtaacgcgct  tgctgcttgg  atgcccgagg    5869

catagactgt  acaaaaaaac  agtcataaca  agccatgaaa  accgccactg  cgccgttacc    5929

accgctgcgt  tcggtcaagg  ttctggacca  gttgcgtgag  cgcatacgct  acttgcatta    5989

cagtttacga  accgaacagg  cttatgtcaa  ctgggttcgt  gccttcatcc  gtttccacgg    6049

tgtgcgtcac  ccggcaacct  tgggcagcag  cgaagtcgag  gcatttctgt  cctggctggc    6109

gaacgagcgc  aaggtttcgg  tctccacgca  tcgtcaggca  ttggcggcct  tgctgttctt    6169

ctacggcaag  gtgctgtgca  cggatctgcc  ctggcttcag  gagatcggta  gacctcggcc    6229

gtcgcggcgc  ttgccggtgg  tgctgacccc  ggatgaagtg  gttcgcatcc  tcggttttct    6289

ggaaggcgag  catcgtttgt  tcgcccagga  ctctagctat  agttctagtg  gttggcctac    6349

gtacccgtag  tggctatggc  agggcttgcc  gccccgacgt  tggctgcgag  ccctgggcct    6409

tcacccgaac  ttggggggttg  gggtggggaa  aaggaagaaa  cgcgggcgta  ttggtcccaa    6469

tggggtctcg  gtggggtatc  gacagagtgc  cagccctggg  accgaacccc  gcgtttatga    6529

acaaacgacc  caacacccgt  gcgttttatt  ctgtcttttt  attgccgtca  tagcgcgggt    6589

tccttccggt  attgtctcct  tccgtgtttc  agttagcctc  ccccatctcc  cggtaccgca    6649

tgcctcgaga  ctgcaggctc  tagattcgaa  agcggccgcg  actagtgagc  tcgtcgacgt    6709

aggcctttga  attccggatc  ctcactcaag  gtcctcatca  gagacggtcc  tgatccagcg    6769

gcccagccga  ccagggggtc  tctgtgttgg  agcattgggt  tttggcttgg  gctttggtag    6829

agcccgcctg  ggattgcgat  gcttcatctc  catcgcagtc  aagagcagat  ctttcatctg    6889

ttcttggttt  gggccacgtc  catggttgat  ttcatagact  ttggcaactt  cgtctatgaa    6949

agcttggggt  ggctctgcct  gtcctggagc  cccgtagatc  gacgtagctg  cccttaggat    7009

ttgttcttct  gatgccaacc  ggctcttctc  tgcatgcacg  tagtctagat  agtcctcgtt    7069

tgggtccggt  atttctcgtt  tgttctgcca  gtactttacc  tggcctgggc  ttggccctcg    7129

gtgcccattg  agtgctaccc  attctggtgt  tgcaaagtag  atgcccatgg  tctccatctt    7189
```

```
ctttgagatc cgtgtgtctt tttccctctg tgcttcctct ggtgtggggc cccgagcctc    7249

cactccgtag cctgctgtcc cgtacttggc cctttgcgac ttgctgcctg cttgtggtgc    7309

gtttgcaaga aaatttcgca tccgatgggc gttcgggtcg ctgagtgcga agttggccat    7369

gtcagtcaca atcccattct cttccagcca catgaacaca ctgagtgcag attggaatag    7429

tgggtccacg ttggctgctg cttccattgc tctgacggca ctctcgagtt cgggggtctc    7489

tttgaactct gatgcagcca ggcgccctg  aaaatacagg ttttcggtcg ttgggatatc    7549

gtaatcgtga tggtgatggt gatggtagta cgacatggtt tcggac                   7595
```

<210> 4
<211> 333
<212> PRT
<213> Artificial sequence

<220>
<223> pVP2-his-VP3 protein

<400> 4

```
Met Thr Asn Leu Ser Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
1               5                   10                  15

Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
                20                  25                  30

Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
            35                  40                  45

Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
        50                  55                  60

Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr
65                  70                  75                  80

Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
                85                  90                  95

Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
            100                 105                 110

Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
        115                 120                 125

Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
        130                 135                 140

Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
145                 150                 155                 160

Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
                165                 170                 175

Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
                180                 185                 190
```

```
Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
        195             200             205

Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly
    210             215             220

Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
225             230             235             240

Ser Val Gly Gly Glu Leu Val Phe Arg Thr Ser Val His Gly Leu Val
            245             250             255

Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile
        260             265             270

Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn
        275             280             285

Leu Met Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro
    290             295             300

Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
305             310             315             320

Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu
            325             330
```

```
<210>   5
<211>   35
<212>   DNA
<213>   Artificial sequence

<220>   Synthetic DNA
<223>   Oligo III primer

<400>   5
gcgcagatct atgacaaacc tgtcagatca aaccc                          35


<210>   6
<211>   34
<212>   DNA
<213>   Artificial sequence

<220>   Synthetic DNA
<223>   Oligo IV primer

<400>   6
gcgcaagctt aggcgagagt cagctgcctt atgc                           34


<210>   7
<211>   9600
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Plasmid pESCURA/pVP2-VP3-GFP
```

<220>
<221> promoter
<222> (5649)..(5859)
<223> Promoter 1 (pVP2)

<220>
<221> promoter
<222> (7402)..(8080)
<223> Promoter 2 (VP3-GFP)

<220>
<221> CDS
<222> (8086)..(9597)
<223> VP3-GFP ORF

<400> 7

```
ggccgcacta gtatcgatgg attacaagga tgacgacgat aagatctgag ctcttaatta      60

acaattcttc gccagaggtt tggtcaagtc tccaatcaag gttgtcggct tgtctacctt     120

gccagaaatt tacgaaaaga tggaaaaggg tcaaatcgtt ggtagatacg ttgttgacac     180

ttctaaataa gcgaatttct tatgatttat gatttttatt attaaataag ttataaaaaa     240

aataagtgta tacaaatttt aaagtgactc ttaggtttta aaacgaaaat cttattctt     300

gagtaactct ttcctgtagg tcaggttgct ttctcaggta tagcatgagg tcgctccaat     360

tcagctgcat taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc     420

ttccgcttcc tcgctcactg actcgctgcg ctcggtcgtt cggctgcggc gagcggtatc     480

agctcactca aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa     540

catgtgagca aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcgtt     600

tttccatagg ctccgccccc ctgacgagca tcacaaaaat cgacgctcaa gtcagaggtg     660

gcgaaacccg acaggactat aaagatacca ggcgtttccc cctggaagct ccctcgtgcg     720

ctctcctgtt ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc cttcgggaag     780

cgtggcgctt tctcatagct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc     840

caagctgggc tgtgtgcacg aacccccgt tcagcccgac cgctgcgcct tatccggtaa     900

ctatcgtctt gagtccaacc cggtaagaca cgacttatcg ccactggcag cagccactgg     960

taacaggatt agcagagcga ggtatgtagg cggtgctaca gagttcttga agtggtggcc    1020

taactacggc tacactagaa ggacagtatt tggtatctgc gctctgctga gccagttac     1080

cttcggaaaa agagttggta gctcttgatc cggcaaacaa accaccgctg gtagcggtgg    1140

tttttttgtt tgcaagcagc agattacgcg cagaaaaaaa ggatctcaag aagatccttt    1200

gatcttttct acggggtctg acgctcagtg gaacgaaaac tcacgttaag ggattttggt .  1260
```

```
catgagatta  tcaaaaagga  tcttcaccta  gatcctttta  aattaaaaat  gaagttttaa     1320

atcaatctaa  agtatatatg  agtaaacttg  gtctgacagt  taccaatgct  taatcagtga     1380

ggcacctatc  tcagcgatct  gtctatttcg  ttcatccata  gttgcctgac  tccccgtcgt     1440

gtagataact  acgatacggg  agggcttacc  atctggcccc  agtgctgcaa  tgataccgcg     1500

agacccacgc  tcaccggctc  cagatttatc  agcaataaac  cagccagccg  gaagggccga     1560

gcgcagaagt  ggtcctgcaa  ctttatccgc  ctccatccag  tctattaatt  gttgccggga     1620

agctagagta  agtagttcgc  cagttaatag  tttgcgcaac  gttgttgcca  ttgctacagg     1680

catcgtggtg  tcacgctcgt  cgtttggtat  ggcttcattc  agctccggtt  cccaacgatc     1740

aaggcgagtt  acatgatccc  ccatgttgtg  caaaaaagcg  gttagctcct  tcggtcctcc     1800

gatcgttgtc  agaagtaagt  tggccgcagt  gttatcactc  atggttatgg  cagcactgca     1860

taattctctt  actgtcatgc  catccgtaag  atgcttttct  gtgactggtg  agtactcaac     1920

caagtcattc  tgagaatagt  gtatgcggcg  accgagttgc  tcttgcccgg  cgtcaatacg     1980

ggataatacc  gcgccacata  gcagaacttt  aaaagtgctc  atcattggaa  aacgttcttc     2040

ggggcgaaaa  ctctcaagga  tcttaccgct  gttgagatcc  agttcgatgt  aacccactcg     2100

tgcacccaac  tgatcttcag  catcttttac  tttcaccagc  gtttctgggt  gagcaaaaac     2160

aggaaggcaa  aatgccgcaa  aaaagggaat  aagggcgaca  cggaaatgtt  gaatactcat     2220

actcttcctt  tttcaatatt  attgaagcat  ttatcagggt  tattgtctca  tgagcggata     2280

catatttgaa  tgtatttaga  aaaataaaca  aataggggtt  ccgcgcacat  ttccccgaaa     2340

agtgccacct  gaacgaagca  tctgtgcttc  attttgtaga  acaaaaatgc  aacgcgagag     2400

cgctaatttt  tcaaacaaag  aatctgagct  gcatttttac  agaacagaaa  tgcaacgcga     2460

aagcgctatt  ttaccaacga  agaatctgtg  cttcattttt  gtaaacaaa   aatgcaacgc     2520

gagagcgcta  atttttcaaa  caagaatct   gagctgcatt  tttacagaac  agaaatgcaa     2580

cgcgagagcg  ctatttttacc  aacaagaat  ctatacttct  tttttgttct  acaaaaatgc     2640

atcccgagag  cgctattttt  ctaacaaagc  atcttagatt  actttttttc  tcctttgtgc     2700

gctctataat  gcagtctctt  gataactttt  tgcactgtag  gtccgttaag  gttagaagaa     2760

ggctactttg  gtgtctattt  tctcttccat  aaaaaaagcc  tgactccact  tcccgcgttt     2820

actgattact  agcgaagctg  cgggtgcatt  ttttcaagat  aaaggcatcc  ccgattatat     2880

tctataccga  tgtggattgc  gcatactttg  tgaacagaaa  gtgatagcgt  tgatgattct     2940

tcattggtca  gaaaattatg  aacggtttct  ctatttgt   ctctatatac  tacgtatagg     3000

aaatgtttac  attttcgtat  tgttttcgat  tcactctatg  aatagttctt  actacaattt     3060
```

```
ttttgtctaa agagtaatac tagagataaa cataaaaaat gtagaggtcg agtttagatg   3120

caagttcaag gagcgaaagg tggatgggta ggttatatag ggatatagca cagagatata   3180

tagcaaagag atacttttga gcaatgtttg tggaagcggt attcgcaata ttttagtagc   3240

tcgttacagt ccggtgcgtt tttggttttt tgaaagtgcg tcttcagagc gcttttggtt   3300

ttcaaaagcg ctctgaagtt cctatacttt ctagagaata ggaacttcgg aataggaact   3360

tcaaagcgtt tccgaaaacg agcgcttccg aaaatgcaac gcgagctgcg cacatacagc   3420

tcactgttca cgtcgcacct atatctgcgt gttgcctgta tatatatata catgagaaga   3480

acggcatagt gcgtgtttat gcttaaatgc gtacttatat gcgtctattt atgtaggatg   3540

aaaggtagtc tagtacctcc tgtgatatta tcccattcca tgcggggtat cgtatgcttc   3600

cttcagcact acccttttagc tgttctatat gctgccactc ctcaattgga ttagtctcat   3660

ccttcaatgc tatcatttcc tttgatattg gatcatacta agaaaccatt attatcatga   3720

cattaaccta taaaaatagg cgtatcacga ggccctttcg tctcgcgcgt ttcggtgatg   3780

acggtgaaaa cctctgacac atgcagctcc cggagacggt cacagcttgt ctgtaagcgg   3840

atgccgggag cagacaagcc cgtcagggcg cgtcagcggg tgttggcggg tgtcggggct   3900

ggcttaacta tgcggcatca gagcagattg tactgagagt gcaccatacc acagcttttc   3960

aattcaattc atcattttttt ttttattctt tttttttgatt tcggtttctt tgaaatttttt   4020

ttgattcggt aatctccgaa cagaaggaag aacgaaggaa ggagcacaga cttagattgg   4080

tatatatacg catatgtagt gttgaagaaa catgaaattg cccagtattc ttaacccaac   4140

tgcacagaac aaaaacctgc aggaaacgaa gataaatcat gtcgaaagct acatataagg   4200

aacgtgctgc tactcatcct agtcctgttg ctgccaagct atttaatatc atgcacgaaa   4260

agcaaacaaa cttgtgtgct tcattggatg ttcgtaccac caaggaatta ctggagttag   4320

ttgaagcatt aggtcccaaa atttgtttac taaaaacaca tgtggatatc ttgactgatt   4380

tttccatgga gggcacagtt aagccgctaa aggcattatc cgccaagtac aattttttac   4440

tcttcgaaga cagaaaattt gctgacattg gtaatacagt caaattgcag tactctgcgg   4500

gtgtatacag aatagcagaa tgggcagaca ttacgaatgc acacggtgtg gtgggcccag   4560

gtattgttag cggtttgaag caggcggcag aagaagtaac aaaggaacct agaggccttt   4620

tgatgttagc agaattgtca tgcaagggct ccctatctac tggagaatat actaagggta   4680

ctgttgacat tgcgaagagc gacaaagatt ttgttatcgg ctttattgct caaagagaca   4740

tgggtggaag agatgaaggt tacgattggt tgattatgac acccggtgtg ggtttagatg   4800

acaagggaga cgcattgggt caacagtata gaaccgtgga tgatgtggtc tctacaggat   4860
```

```
ctgacattat tattgttgga agaggactat ttgcaaaggg aagggatgct aaggtagagg   4920

gtgaacgtta cagaaaagca ggctgggaag catatttgag aagatgcggc cagcaaaact   4980

aaaaaactgt attataagta aatgcatgta tactaaactc acaaattaga gcttcaattt   5040

aattatatca gttattaccc tatgcggtgt gaaataccgc acagatgcgt aaggagaaaa   5100

taccgcatca ggaaattgta aacgttaata ttttgttaaa attcgcgtta aattttttgtt  5160

aaatcagctc attttttaac caataggccg aaatcggcaa aatcccttat aaatcaaaag   5220

aatagaccga gatagggttg agtgttgttc cagtttggaa caagagtcca ctattaaaga   5280

acgtggactc caacgtcaaa gggcgaaaaa ccgtctatca gggcgatggc ccactacgtg   5340

aaccatcacc ctaatcaagt tttttggggt cgaggtgccg taaagcacta aatcggaacc   5400

ctaaagggag cccccgattt agagcttgac ggggaaagcc ggcgaacgtg gcgagaaagg   5460

aagggaagaa agcgaaagga gcgggcgcta gggcgctggc aagtgtagcg gtcacgctgc   5520

gcgtaaccac cacacccgcc gcgcttaatg cgccgctaca gggcgcgtcg cgccattcgc   5580

cattcaggct gcgcaactgt tgggaagggc gatcggtgcg ggcctcttcg ctattacgcc   5640

agctggatct tcgagcgtcc caaaaccttc tcaagcaagg ttttcagtat aatgttacat   5700

gcgtacacgc gtctgtacag aaaaaaaaga aaatttgaa atataaataa cgttcttaat   5760

actaacataa ctataaaaaa ataaataggg acctagactt caggttgtct aactccttcc   5820

ttttcggtta gagcggatct tagctagccg cggtaccaag cttaggcgag agtcagctgc   5880

cttatcggc ctgaggcagc tcttgctttt cctgacgcgg ctcgagcagt tcctgaagcg   5940

gcctgggcct catcgcccag caggtagtct acaccttccc caattgcatg ggctagggga   6000

gcggcaggtg ggaacaatgt ggagaccacc ggcacagcta tcctccttat ggcccggatt   6060

atgtctttga agccgaatgc tcctgcaatc ttcaggggag agttgaggtc ggccacctcc   6120

atgaagtatt cacgaaagtc agtgtactcc cttgttggcc agacggtctt gatgccaaga   6180

cggtccctct cactcagtat caattttgtg tagttcatgg ctcctgggtc aaatcggccg   6240

tattctgtaa ccaggttctt tgctagttca ggatttggga tcagctcgaa gttgctcacc   6300

ccagcgaccg taacgacgga tcctgttgcc actctttcgt aggccactag cgtgacggga   6360

cggagggccc ctggatagtt gccaccatgg atcgtcactg ctaggctccc tcttgccgac   6420

catgacatct gatcccctgc ctgaccacca cttttggagg tcactatctc cagtttgatg   6480

gatgtgattg gctgggttat ctcgtttgtt ggaatcacaa gattgaatgg cataaggttg   6540

tcggtgccgg tcgtcagccc attgtttgcg gccacagccc tggtgattac cgttgtccca   6600

tcaaagccta tgaggtagat ggtggcgccc agtacaaggc cgtggacgct tgttcgaaac   6660
```

```
acgagctctc ccccaacgct gaggcttgtg atggcatcaa tgttggctga gaacagtgtg    6720

attgttaccc cacctggttg gtactgtgat gagaattggt aatcatcggc tgcagttatg    6780

gtgtagactc tgggcctgtc actgctgtca catgtggcta ccattttttgg gtcaagccct   6840

attgcgggaa tggggtcacc aagcctcaca tacccaagat catatgatgt gggtaagctg    6900

aggacggtga ccccttcccc tactaggacg ttcccaattt tgtcgttgat gttggctgtt    6960

gcagacatca acccattgta gctaacatct gtcagttcac tcaggcttcc ttggaaggtc    7020

acggcgttta tggtgccgtt tagtgcataa acgccaccag gaagtgtgct tgacctcact    7080

gtgagactcc gactcactag cctgcagtag ttgtaactgg ccggtaggtt ctgggcagtc    7140

aggagcatct gatcgaactt gtagttccca ttgccctgca gtgtgtagtg agcacccaca    7200

attgagccag ggaatccagg gaaaaagaca attagccctg accctgtgtc ccccacagtc    7260

aaattgtagg tcgaggtctc tgacctgaga gtgtgcttct ccagggtgtc gtccggaatg    7320

gacgccggtc cggttgttgg catcagaagg ctccgtatga acggaacaat ctgctgggtt    7380

tgatctgaca ggtttgtcat agatccgggg ttttttctcc ttgacgttaa agtatagagg    7440

tatattaaca attttttgtt gatactttta ttacatttga ataagaagta atacaaaccg    7500

aaaatgttga aagtattagt taaagtggtt atgcagtttt tgcatttata tatctgttaa    7560

tagatcaaaa atcatcgctt cgctgattaa ttaccccaga aataaggcta aaaaactaat    7620

cgcattatca tcctatggtt gttaatttga ttcgttcatt tgaaggtttg tggggccagg    7680

ttactgccaa ttttttcctct tcataaccat aaaagctagt attgtagaat ctttattgtt    7740

cggagcagtg cggcgcgagg cacatctgcg tttcaggaac gcgaccggtg aagacgagga    7800

cgcacggagg agagtcttcc ttcggagggc tgtcacccgc tcggcggctt ctaatccgta    7860

cttcaatata gcaatgagca gttaagcgta ttactgaaag ttccaaagag aaggttttttt   7920

taggctaaga taatggggct ctttacattt ccacaacata taagtaagat tagatatgga    7980

tatgtatatg gatatgtata tggtggtaat gccatgtaat atgattatta aacttctttg    8040

cgtccatcca aaaaaaaagt aagaatttttt gaaaattcga attcg atg gct gca tca    8097
                                                     Met Ala Ala Ser
                                                      1

gag ttc aaa gag acc ccc gaa ctc gag agt gcc gtc aga gca atg gaa        8145
Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala Val Arg Ala Met Glu
 5              10              15              20

gca gca gcc aac gtg gac cca cta ttc caa tct gca ctc agt gtg ttc        8193
Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser Ala Leu Ser Val Phe
             25              30              35

atg tgg ctg gaa gag aat ggg att gtg act gac atg gcc aac ttc gca        8241
```

```
    Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala Asn Phe Ala
             40                  45              50

    ctc agc gac ccg aac gcc cat cgg atg cga aat ttt ctt gca aac gca       8289
    Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn Phe Leu Ala Asn Ala
             55                  60                  65

    cca caa gca ggc agc aag tcg caa agg gcc aag tac ggg aca gca ggc       8337
    Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly Thr Ala Gly
         70                  75                  80

    tac gga gtg gag gct cgg ggc ccc aca cca gag gaa gca cag agg gaa       8385
    Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala Gln Arg Glu
    85                  90                  95                 100

    aaa gac aca cgg atc tca aag aag atg gag acc atg ggc atc tac ttt       8433
    Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly Ile Tyr Phe
                     105                 110                 115

    gca aca cca gaa tgg gta gca ctc aat ggg cac cga ggg cca agc cca       8481
    Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly Pro Ser Pro
                 120                 125                 130

    ggc cag gta aag tac tgg cag aac aaa cga gaa ata ccg gac cca aac       8529
    Gly Gln Val Lys Tyr Trp Gln Asn Lys Arg Glu Ile Pro Asp Pro Asn
             135                 140                 145

    gag gac tat cta gac tac gtg cat gca gag aag agc cgg ttg gca tca       8577
    Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys Ser Arg Leu Ala Ser
         150                 155                 160

    gaa gaa caa atc cta agg gca gct acg tcg atc tac ggg gct cca gga       8625
    Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile Tyr Gly Ala Pro Gly
    165                 170                 175                 180

    cag gca gag cca ccc caa gct ttc ata gac gaa gtt gcc aaa gtc tat       8673
    Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala Lys Val Tyr
                     185                 190                 195

    gaa atc aac cat gga cgt ggc cca aac caa gaa cag atg aaa gat ctg       8721
    Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met Lys Asp Leu
                 200                 205                 210

    ctc ttg act gcg atg gag atg aag cat cgc aat ccc agg cgg gct cta       8769
    Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg Arg Ala Leu
             215                 220                 225

    cca aag ccc aag cca aaa ccc aat gct cca aca cag aga ccc cct ggt       8817
    Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln Arg Pro Pro Gly
         230                 235                 240

    cgg ctg ggc cgc tgg atc agg acc gtc tct gat gag gac ctt gag gga       8865
    Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp Leu Glu Gly
    245                 250                 255                 260

    tcc atc gcc acc atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg       8913
    Ser Ile Ala Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                     265                 270                 275

    gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc       8961
```

```
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            280                 285                 290

agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc    9009
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        295                 300                 305

ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc    9057
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    310                 315                 320

ctc gtg acc acc ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc    9105
Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
325                 330                 335                 340

gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc    9153
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                345                 350                 355

tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag    9201
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            360                 365                 370

acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc    9249
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        375                 380                 385

gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac    9297
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    390                 395                 400

aag ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc gac    9345
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
405                 410                 415                 420

aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc    9393
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                425                 430                 435

gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc    9441
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            440                 445                 450

atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc    9489
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        455                 460                 465

cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc    9537
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    470                 475                 480

ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag    9585
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
485                 490                 495                 500

ctg tac aag taa agc                                                 9600
Leu Tyr Lys
```

```
<210>  8
<211>  503
<212>  PRT
<213>  Artificial sequence

<220>
<223>  pVP2-VP3-GFP protein

<400>  8
Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala Val
1               5                   10                  15

Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser Ala
                20              25                  30

Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met
            35                  40                  45

Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn Phe
        50              55                  60

Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr
65                  70                  75                  80

Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu
                85                  90                  95

Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met
                100                 105                 110

Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg
            115                 120                 125

Gly Pro Ser Pro Gly Gln Val Lys Tyr Trp Gln Asn Lys Arg Glu Ile
        130                 135                 140

Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys Ser
145                 150                 155                 160

Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile Tyr
                165                 170                 175

Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val
            180                 185                 190

Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln
            195                 200                 205

Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro
    210                 215                 220

Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln
225                 230                 235                 240

Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu
            245                 250                 255

Asp Leu Glu Gly Ser Ile Ala Thr Met Val Ser Lys Gly Glu Glu Leu
            260                 265                 270
```

```
Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
        275             280             285

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
        290             295             300

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
305             310             315             320

Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln Cys Phe
            325             330             335

Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
        340             345             350

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
        355             360             365

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
    370             375             380

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
385             390             395             400

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
            405             410             415

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
            420             425             430

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
        435             440             445

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
    450             455             460

Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
465             470             475             480

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
            485             490             495

Gly Met Asp Glu Leu Tyr Lys
            500
```

```
<210>  9
<211>  33
<212>  DNA
<213>  Artificial sequence

<220>  Synthetic DNA
<223>  Oligo V primer

<400>  9
gcgcgaattc gatggcatca gagttcaaag aga                              33

<210>  10
<211>  32
```

```
<212>   DNA
<213>   Artificial sequence

<220>   Synthetic DNA
<223>   Oligo VI primer

<400>   10
cgcggatccc tcaaggtcct catcagagac gg                                    32


<210>   11
<211>   36
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Oligo CD8 A primer

<400>   11
aacgaggaca gttatgtccc aagcgcagaa caaata                                36


<210>   12
<211>   36
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Oligo CD8 B primer

<400>   12
tatttgttct gcgcttggga cataactgtc ctcgtt                                36

<210>   13
<211>   5676
<212>   DNA
<213>   Artificial sequence

<220>
<223>   Plasmid pFB/his-CD8-VP3

<220>
<221>   promoter
<222>   (1)..(129)
<223>   Polyhedrin promoter

<220>
<221>   CDS
<222>   (147)..(1043)
<223>   His-CD8-VP3 ORF

<220>
<221>   CDS
<222>   (222)..(257)
<223>   His-CD8 ORF

<400>   13
atcatggaga taattaaaat gataaccatc tcgcaaataa ataagtattt tactgttttc     60

gtaacagttt tgtaataaaa aaacctataa atattccgga ttattcatac cgtcccacca    120
```

```
tcgggcgcgg atctcggtcc gaaacc atg tcg tac tac cat cac cat cac cat      173
                             Met Ser Tyr Tyr His His His His His
                             1             5

cac gat tac gat atc cca acg acc gaa aac ctg tat ttt cag ggc gcg      221
His Asp Tyr Asp Ile Pro Thr Thr Glu Asn Leu Tyr Phe Gln Gly Ala
10              15              20              25

aac gag gac agt tat gtc cca agc gca gaa caa ata gcc gcc atg gct      269
Asn Glu Asp Ser Tyr Val Pro Ser Ala Glu Gln Ile Ala Ala Met Ala
            30              35              40

gca tca gag ttc aaa gag acc ccc gaa ctc gag agt gcc gtc aga gca      317
Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu Glu Ser Ala Val Arg Ala
        45              50              55

atg gaa gca gca gcc aac gtg gac cca cta ttc caa tct gca ctc agt      365
Met Glu Ala Ala Ala Asn Val Asp Pro Leu Phe Gln Ser Ala Leu Ser
        60              65              70

gtg ttc atg tgg ctg gaa gag aat ggg att gtg act gac atg gcc aac      413
Val Phe Met Trp Leu Glu Glu Asn Gly Ile Val Thr Asp Met Ala Asn
    75              80              85

ttc gca ctc agc gac ccg aac gcc cat cgg atg cga aat ttt ctt gca      461
Phe Ala Leu Ser Asp Pro Asn Ala His Arg Met Arg Asn Phe Leu Ala
90              95              100             105

aac gca cca caa gca ggc agc aag tcg caa agg gcc aag tac ggg aca      509
Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln Arg Ala Lys Tyr Gly Thr
            110             115             120

gca ggc tac gga gtg gag gct cgg ggc ccc aca cca gag gaa gca cag      557
Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro Thr Pro Glu Glu Ala Gln
            125             130             135

agg gaa aaa gac aca cgg atc tca aag aag atg gag acc atg ggc atc      605
Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr Met Gly Ile
        140             145             150

tac ttt gca aca cca gaa tgg gta gca ctc aat ggg cac cga ggg cca      653
Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His Arg Gly Pro
        155             160             165

agc cca ggc cag gta aag tac tgg cag aac aaa cga gaa ata ccg gac      701
Ser Pro Gly Gln Val Lys Tyr Trp Gln Asn Lys Arg Glu Ile Pro Asp
170             175             180             185

cca aac gag gac tat cta gac tac gtg cat gca gag aag agc cgg ttg      749
Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys Ser Arg Leu
            190             195             200

gca tca gaa gaa caa atc cta agg gca gct acg tcg atc tac ggg gct      797
Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile Tyr Gly Ala
            205             210             215
```

```
cca gga cag gca gag cca ccc caa gct ttc ata gac gaa gtt gcc aaa        845
Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu Val Ala Lys
        220             225                 230

gtc tat gaa atc aac cat gga cgt ggc cca aac caa gaa cag atg aaa        893
Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu Gln Met Lys
        235             240                 245

gat ctg ctc ttg act gcg atg gag atg aag cat cgc aat ccc agg cgg        941
Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn Pro Arg Arg
250             255                 260                 265

gct cta cca aag ccc aag cca aaa ccc aat gct cca aca cag aga ccc        989
Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr Gln Arg Pro
                270             275                 280

cct ggt cgg ctg ggc cgc tgg atc agg acc gtc tct gat gag gac ctt       1037
Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp Glu Asp Leu
                285                 290                 295

gag tga ggatccggaa ttcaaaggcc tacgtcgacg agctcactag tcgcggccgc        1093
Glu
```

```
tttcgaatct agagcctgca gtctcgaggc atgcggtacc aagcttgtcg agaagtacta     1153

gaggatcata atcagccata ccacatttgt agaggtttta cttgctttaa aaaacctccc     1213

acacctcccc ctgaacctga aacataaaat gaatgcaatt gttgttgtta acttgtttat     1273

tgcagcttat aatggttaca aataaagcaa tagcatcaca aatttcacaa ataaagcatt     1333

tttttcactg cattctagtt gtggtttgtc caaactcatc aatgtatctt atcatgtctg     1393

gatctgatca ctagatctgc ctaggagatc cgaaccagat aagtgaaatc tagttccaaa     1453

ctattttgtc atttttaatt ttcgtattag cttacgacgc tacacccagt tcccatctat     1513

tttgtcactc ttccctaaat aatccttaaa aactccattt ccacccctcc cagttcccaa     1573

ctattttgtc cgcccacagc ggggcatttt cttcctgtt atgttttaa tcaaacatcc      1633

tgccaactcc atgtgacaaa ccgtcatctt cggctacttt ttctctgtca cagaatgaaa    1693

atttttctgt catctcttcg ttattaatgt ttgtaattga ctgaatatca acgcttattt    1753

gcagcctgaa tggcgaatgg gacgcgccct gtagcggcgc attaagcgcg gcgggtgtgg    1813

tggttacgcg cagcgtgacc gctacacttg ccagcgccct agcgcccgct cctttcgctt    1873

tcttcccttc ctttctcgcc acgttcgccg gctttccccg tcaagctcta atcggggggc    1933

tcccttacgg gttccgattt agtgctttac ggcacctcga ccccaaaaaa cttgattagg    1993

gtgatggttc acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg    2053

agtccacgtt ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct    2113

cggtctattc ttttgattta taagggattt tgccgatttc ggcctattgg ttaaaaaatg    2173
```

```
agctgattta acaaaaattt aacgcgaatt ttaacaaaat attaacgttt acaatttcag   2233

gtggcacttt tcggggaaat gtgcgcggaa cccctatttg tttatttttc taaatacatt   2293

caaatatgta tccgctcatg agacaataac cctgataaat gcttcaataa tattgaaaaa   2353

ggaagagtat gagtattcaa catttccgtg tcgcccttat tccctttttt gcggcatttt   2413

gccttcctgt ttttgctcac ccagaaacgc tggtgaaagt aaaagatgct gaagatcagt   2473

tgggtgcacg agtgggttac atcgaactgg atctcaacag cggtaagatc cttgagagtt   2533

ttcgccccga agaacgtttt ccaatgatga gcacttttaa agttctgcta tgtggcgcgg   2593

tattatcccg tattgacgcc gggcaagagc aactcggtcg ccgcatacac tattctcaga   2653

atgacttggt tgagtactca ccagtcacag aaaagcatct tacggatggc atgacagtaa   2713

gagaattatg cagtgctgcc ataaccatga gtgataacac tgcggccaac ttacttctga   2773

caacgatcgg aggaccgaag gagctaaccg cttttttgca acatggggg gatcatgtaa   2833

ctcgccttga tcgttgggaa ccggagctga atgaagccat accaaacgac gagcgtgaca   2893

ccacgatgcc tgtagcaatg gcaacaacgt tgcgcaaact attaactggc gaactactta   2953

ctctagcttc ccggcaacaa ttaatagact ggatggaggc ggataaagtt gcaggaccac   3013

ttctgcgctc ggcccttccg gctggctggt ttattgctga taaatctgga gccggtgagc   3073

gtgggtctcg cggtatcatt gcagcactgg ggccagatgg taagccctcc cgtatcgtag   3133

ttatctacac gacggggagt caggcaacta tggatgaacg aaatagacag atcgctgaga   3193

taggtgcctc actgattaag cattggtaac tgtcagacca agtttactca tatatacttt   3253

agattgattt aaaacttcat ttttaattta aaaggatcta ggtgaagatc cttttttgata   3313

atctcatgac caaaatccct taacgtgagt tttcgttcca ctgagcgtca gacccccgtag   3373

aaaagatcaa aggatcttct tgagatcctt tttttctgcg cgtaatctgc tgcttgcaaa   3433

caaaaaaacc accgctacca gcggtggttt gtttgccgga tcaagagcta ccaactcttt   3493

ttccgaaggt aactggcttc agcagagcgc agataccaaa tactgtcctt ctagtgtagc   3553

cgtagttagg ccaccacttc aagaactctg tagcaccgcc tacatacctc gctctgctaa   3613

tcctgttacc agtggctgct gccagtggcg ataagtcgtg tcttaccggg ttggactcaa   3673

gacgatagtt accggataag cgcagcggt cgggctgaac ggggggttcg tgcacacagc    3733

ccagcttgga gcgaacgacc tacaccgaac tgagatacct acagcgtgag cattgagaaa   3793

gcgccacgct tcccgaaggg agaaaggcgg acaggtatcc ggtaagcggc agggtcggaa   3853

caggagagcg cacgagggag cttccagggg gaaacgcctg gtatctttat agtcctgtcg   3913

ggtttcgcca cctctgactt gagcgtcgat ttttgtgatg ctcgtcaggg gggcggagcc   3973
```

22

```
tatggaaaaa cgccagcaac gcggcctttt tacggttcct ggccttttgc tggccttttg    4033

ctcacatgtt ctttcctgcg ttatcccctg attctgtgga taaccgtatt accgcctttg    4093

agtgagctga taccgctcgc cgcagccgaa cgaccgagcg cagcgagtca gtgagcgagg    4153

aagcggaaga gcgcctgatg cggtattttc tccttacgca tctgtgcggt atttcacacc    4213

gcagaccagc cgcgtaacct ggcaaaatcg gttacggttg agtaataaat ggatgccctg    4273

cgtaagcggg tgtgggcgga caataaagtc ttaaactgaa caaaatagat ctaaactatg    4333

acaataaagt cttaaactag acagaatagt tgtaaactga atcagtcca gttatgctgt     4393

gaaaaagcat actggacttt tgttatggct aaagcaaact cttcattttc tgaagtgcaa    4453

attgcccgtc gtattaaaga ggggcgtggc caagggcatg gtaaagacta tattcgcggc    4513

gttgtgacaa tttaccgaac aactccgcgg ccgggaagcc gatctcggct tgaacgaatt    4573

gttaggtggc ggtacttggg tcgatatcaa agtgcatcac ttcttcccgt atgcccaact    4633

ttgtatagag agccactgcg ggatcgtcac cgtaatctgc ttgcacgtag atcacataag    4693

caccaagcgc gttggcctca tgcttgagga gattgatgag cgcggtggca atgccctgcc    4753

tccggtgctc gccggagact gcgagatcat agatatagat ctcactacgc ggctgctcaa    4813

acctgggcag aacgtaagcc gcgagagcgc caacaaccgc ttcttggtcg aaggcagcaa    4873

gcgcgatgaa tgtcttacta cggagcaagt tcccgaggta atcggagtcc ggctgatgtt    4933

gggagtaggt ggctacgtct ccgaactcac gaccgaaaag atcaagagca gcccgcatgg    4993

atttgacttg gtcagggccg agcctacatg tgcgaatgat gcccatactt gagccaccta    5053

actttgtttt agggcgactg ccctgctgcg taacatcgtt gctgctgcgt aacatcgttg    5113

ctgctccata acatcaaaca tcgacccacg gcgtaacgcg cttgctgctt ggatgcccga    5173

ggcatagact gtacaaaaaa acagtcataa caagccatga aaaccgccac tgcgccgtta    5233

ccaccgctgc gttcggtcaa ggttctggac cagttgcgtg agcgcatacg ctacttgcat    5293

tacagtttac gaaccgaaca ggcttatgtc aactgggttc gtgccttcat ccgtttccac    5353

ggtgtgcgtc acccggcaac cttgggcagc agcgaagtcg aggcatttct gtcctggctg    5413

gcgaacgagc gcaaggtttc ggtctccacg catcgtcagg cattggcggc cttgctgttc    5473

ttctacggca aggtgctgtg cacggatctg ccctggcttc aggagatcgg aagacctcgg    5533

ccgtcgcggc gcttgccggt ggtgctgacc ccggatgaag tggttcgcat cctcggtttt    5593

ctggaaggcg agcatcgttt gttcgcccag gactctagct atagttctag tggttggcta    5653

cgtatactcc ggaatattaa tag                                            5676
```

```
<210>   14
<211>   298
<212>   PRT
<213>   Artificial sequence

<220>
<223>   his-CD8-VP3 protein

<400>   14

Met Ser Tyr Tyr His His His His His His Asp Tyr Asp Ile Pro Thr
1               5                   10                  15

Thr Glu Asn Leu Tyr Phe Gln Gly Ala Asn Glu Asp Ser Tyr Val Pro
                20              25                  30

Ser Ala Glu Gln Ile Ala Ala Met Ala Ala Ser Glu Phe Lys Glu Thr
            35              40                  45

Pro Glu Leu Glu Ser Ala Val Arg Ala Met Glu Ala Ala Ala Asn Val
        50              55              60

Asp Pro Leu Phe Gln Ser Ala Leu Ser Val Phe Met Trp Leu Glu Glu
65              70              75                  80

Asn Gly Ile Val Thr Asp Met Ala Asn Phe Ala Leu Ser Asp Pro Asn
                85              90                  95

Ala His Arg Met Arg Asn Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser
            100             105             110

Lys Ser Gln Arg Ala Lys Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala
        115             120             125

Arg Gly Pro Thr Pro Glu Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile
        130             135             140

Ser Lys Lys Met Glu Thr Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp
145                 150             155             160

Val Ala Leu Asn Gly His Arg Gly Pro Ser Pro Gly Gln Val Lys Tyr
                165             170             175

Trp Gln Asn Lys Arg Glu Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp
            180             185             190

Tyr Val His Ala Glu Lys Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu
        195             200             205

Arg Ala Ala Thr Ser Ile Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro
        210             215             220

Gln Ala Phe Ile Asp Glu Val Ala Lys Val Tyr Glu Ile Asn His Gly
225             230             235             240

Arg Gly Pro Asn Gln Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met
            245             250             255
```

```
Glu Met Lys His Arg Asn Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro
             260                 265             270

Lys Pro Asn Ala Pro Thr Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp
         275             280             285

Ile Arg Thr Val Ser Asp Glu Asp Leu Glu
    290             295
```